

AMENDMENTS TO THE SPECIFICATION

Please replace the first paragraph on page 1 of the specification with the following paragraph:

This application is a division of pending U.S. Patent Application Serial No. 09/781,814, filed February 12, 2001, which claims benefit of U.S. Provisional Patent Application Serial No. 60/227,966, filed on August 25, 2000, and U.S. Provisional Patent Application Serial No. 60/227,902, filed on August 25, 2000, each of which is incorporated by reference herein in its entirety.

Please replace the paragraph at page 5, lines 21-22 with the following paragraph:

FIG. 6 illustrates an exemplary embodiment of a computer system useful for implementing the methods of the present invention. Illustrated is computer system 601 having the following components: processor unit 602; main memory 603; mass storage unit 604; user interface device 605; graphical input device 606; network link 607; printer 608; software component 610 (operating system); software component 611 (programming languages that can be used to program the analytic methods of the invention); and software component 612 (analytic methods of the present invention, preferably programmed in a procedural language or symbolic package).

Please replace the paragraph at page 7, line 29 to page 8, line 12 with the following paragraph:

FIGS. 13A-[[C]]E depicts depict an exemplary use of screening arrays using expression data from multiple conditions to validate exons and define gene boundaries on chromosome 22. FIG. 13A depicts a pseudo-color an array image showing \log_{10} expression ratios (Red/Green) for each of the ~8,000 exons (x-axis) across the 69 fluor reversed experiments (y-axis). In this Figure, green downregulation of the Cy3 channel relative to the Cy5 channel is represented generally as lighter shades of gray; [[red]] upregulation of the Cy3 channel relative to the Cy5 channel is represented generally as darker shades of gray. A brief description of sixty-nine two-condition experiments is listed on the right side of the image along with numbers that serve as reference points for FIGS. 13B-E. FIG. 13B depicts an expanded region that includes a known gene, SERPIND1 (Accession No. NM_000185). The experiments on the y-axis are clustered to emphasize how co-regulation across diverse experiments can be used to group exons into genes. The vertical white lines show the boundaries predicted by the gene finding algorithm using scanning data. FIG. 13C shows an expanded region containing a set of co-regulated exons from another known gene, G22P1 (Accession No. NM_001469). A potential false exon prediction made by the Genscan prediction program is indicated by the arrow. FIG. 13D shows an expanded region verified

gene that collapses two Unigene EST clusters, HS.269963 and HS.14587, into a single transcript. FIG. 13E shows an expanded region containing a verified gene possessing six exons that are part of a novel transcript that is expressed in the testis. Arrows indicate the position of the two experiments involving testis RNA samples.